```
         1                                              50
rhimi    SIDGGIRAAT SQEINELTYY TTLSANSYCR TVIPGA...T WDC..IHCDA
rhidl    SDGGKVVAAT TAQIQEFTKY AGIAATAYCR SVVPGN...K WDC..VQCQK
SP400    ------EVS QDLFNQFNLF AQYSAAAYCG KNNDAPAGTN ITCTGNACPE
Pcl      ------DVS TSELDQFEFW VQYAAASYYE ADYTAQVGDK LSCSKGNCPE
FoLnp11  -----AVGVT TTDFSNFKFY IQHGAAAYC. .NSEAAAGSK ITCSNNGCPT

         51                                             100
rhimi    TE..DLKIIK TWS.TLIYDT NAMVARGDSE KTIYIVFRGS SSIRNWIADL
rhidl    WV.PDGKIIT TFT.SLLSDT NGYVLRSDKQ KTIYLVFRGT NSFRSAITDI
SP400    VEKADATFLY SFEDSGVGDV TGFLALDNTN KLIVLSFRGS RSIENWIGNL
Pcl      VEATGATVSY DFSDSTITDT AGYIAVDHTN SAVVLAFRGS YSVRNWVADA
FoLnp11  VQGNGATIVT SFVG.SKTGI GGYVATDSAR KEIVVSFRGS INIRNWLTNL

         101                                            150
rhimi    TFVPVSY.PP VSGTKVHKGF LDSYGEVQNE LVATVLDQFK QYPSYKVAVT
rhidl    VFNFSDY.KP VKGAKVHAGF LSSYEQVVND YFPVVQEQLT AHPTYKVIVT
SP400    NFDLKEINDI CSGCRGHDGF TSSWRSVADT LRQKVEDAVR EHPDYRVVFT
Pcl      TFVHTNP.GL CDGCLAELGF WSSWKLVRDD IIKELKEVVA QNPNYELVVV
FoLnp11  DFGQEDC.SL VSGCGVHSGF QRAWNEISSQ ATAAVASARK ANPSFNVIST

         151                                            200
rhimi    GHSLGGATAL LCALDLYQRE EGLSSSNLFL YTQGQPRVGD PAFANYVVST
rhidl    GHSLGGAQAL LAGMDLYQRE PRLSPKNLSI FTVGGPRVGN PTFAYYVEST
SP400    GHSLGGALAT VAGADLRGN. .GY...DIDV FSYGAPRVGN RAFAEFLTVQ
Pcl      GHSLGAAVAT LAATDLRGK. .GYP..SAKL YAYASPRVGN AALAKYITAQ
FoLnp11  GHSLGGAVAV LAAANLRVG. .GT...PVDI YTYGSPRVGN AQLSAFVSNQ

         201                                            250
rhimi    G.IPYRRTVN ERDIVPHLPP AAFGFLHAGE EYWITD.NSP ......ETVQ
rhidl    G.IPFQRTVH KRDIVPHVPP QSFGFLHPGV ESWIKS.GT. ......SNVQ
SP400    TGGTLYRITH TNDIVPRLPP REFGYSHSSP EYWIKS.GTL V.PVTRNDIV
Pcl      G..NNFRFTH TNDPVKLPL LSMGYVHVSP EYWITS.PNN A.TVSTSDIK
FoLnp11  A.GGEYRVTH ADDPVPRLPP LIFGYRHTTP EFWLSGGGGD KVDYTISDVK

         251                                            300
rhimi    VCTSDLETSD CSNSIVPFT. .SVLDHLSYF GINTGLCT-- ----------
rhidl    ICTSEIETKD CSNSIVPFT. .SILDHLSYF DINEGSCL-- ----------
SP400    KIEGID.ATG GNNQP.NIP. .DIPAHLWYF .GLIGTCL-- ----------
Pcl      VIDGDV.SFD GNTGTGLPLL TDFEAHIWYF .VQVDAGKGP GLPFKRV---
FoLnp11  VCEGAA.NLG CNGGT.LGL. .DIAAHLHYF .QATDACNAG GFSWRRYRSA

         301                            338
rhimi    ---------- ---------- ---------- -----...
rhidl    ---------- ---------- ---------- -----...
SP400    ---------- ---------- ---------- -----...
Pcl      ---------- ---------- ---------- -----...
FoLnp11  ESVDKRATMT DAELEKKLNS YVQMDKEYVK NNQARS..
```

Fig. 1

Alignment of lipase sequences